

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 01:06:59 ; Search time 755.06 Seconds
(without alignments)
24.980 Million cell updates/sec

Title: us-09-851-670-13

Sequence: 1 caccgcctcttcgcacatgga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N.Geneseq_1101:*

1:	/SID2/gcgdata/geneseq/geneseq/NA1980.DAT:*
2:	/SID2/gcgdata/geneseq/geneseq/NA1981.DAT:*
3:	/SID2/gcgdata/geneseq/geneseq/NA1982.DAT:*
4:	/SID2/gcgdata/geneseq/geneseq/NA1983.DAT:*
5:	/SID2/gcgdata/geneseq/geneseq/NA1984.DAT:*
6:	/SID2/gcgdata/geneseq/geneseq/NA1985.DAT:*
7:	/SID2/gcgdata/geneseq/geneseq/NA1986.DAT:*
8:	/SID2/gcgdata/geneseq/geneseq/NA1987.DAT:*
9:	/SID2/gcgdata/geneseq/geneseq/NA1988.DAT:*
10:	/SID2/gcgdata/geneseq/geneseq/NA1989.DAT:*
11:	/SID2/gcgdata/geneseq/geneseq/NA1990.DAT:*
12:	/SID2/gcgdata/geneseq/geneseq/NA1991.DAT:*
13:	/SID2/gcgdata/geneseq/geneseq/NA1992.DAT:*
14:	/SID2/gcgdata/geneseq/geneseq/NA1993.DAT:*
15:	/SID2/gcgdata/geneseq/geneseq/NA1994.DAT:*
16:	/SID2/gcgdata/geneseq/geneseq/NA1995.DAT:*
17:	/SID2/gcgdata/geneseq/geneseq/NA1996.DAT:*
18:	/SID2/gcgdata/geneseq/geneseq/NA1997.DAT:*
19:	/SID2/gcgdata/geneseq/geneseq/NA1998.DAT:*
20:	/SID2/gcgdata/geneseq/geneseq/NA1999.DAT:*
21:	/SID2/gcgdata/geneseq/geneseq/NA2000.DAT:*
22:	/SID2/gcgdata/geneseq/geneseq/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	15.2	69.1	24	AA041807	Baculovirus C2 com
2	14.6	66.4	45	AA046031	BCG derived synth
3	14.6	66.4	51	AA077485	Human Gln synthase
4	14.2	64.5	38	AA063755	PCR primer used to
5	13.6	61.8	51	AA013947	Der pII B cell epi
6	13	59.1	28	AA258426	PCR primer used in
7	13	59.1	28	AA258428	PCR primer used in
8	13	59.1	37	AA023269	Cytomegalovirus PC
9	13	59.1	51	AA077484	Human Gln synthase
10	12.8	58.2	17	AA017182	ATy1 hydrocarbon n
11	12.6	57.3	24	AA010088	K-ras LDR oligonuc

C	12	12.6	57.3	24	AA087183	Fibroblast growth
C	13	12.6	57.3	37	AA033266	Cytomegalovirus PC
C	14	12.4	56.4	32	AA033699	Mycobacterium heat
C	15	12.4	56.4	42	AA028152	Primer #5. Uniden
C	16	12.4	56.4	47	AA026756	Human map-related
C	17	12.4	56.4	47	AA026934	Human map-related
C	18	12.4	56.4	51	AA017212	Human clone cg4396
C	19	12.4	56.4	51	AA010912	Human SNP flanking
C	20	12.2	55.5	20	AA011310	Human ANK gene PCR
C	21	12.2	55.5	21	AA018396	Synthetic HIV-1 PC
C	22	12.2	55.5	27	AA010678	Rat Fas ligand-lik
C	23	12.2	55.5	27	AA087667	Rat T4 liver func
C	24	12.2	55.5	30	AA026520	Cross-over linker
C	25	12.2	55.5	36	AA023101	HIV-1 DNA synthesis
C	26	12.2	55.5	39	AA018870	Maize SSR oligonuc
C	27	12.2	55.5	41	AA050620	Brassica sp. polym
C	28	12.2	55.5	42	AA059413	Human papillomavir
C	29	12.2	55.5	45	AA062014	Human beta foillcl
C	30	12.2	55.5	47	AA066472	Human map-related
C	31	12.2	55.5	50	AA032005	Flax SAD gene prom
C	32	12.2	55.5	50	AA032153	Synthetic plasmid
C	33	12.2	55.5	50	AA032079	Synthetic plasmid
C	34	12.2	55.5	51	AA076322	Human native extra
C	35	12	54.5	20	AA020597	PCR primer used to
C	36	12	54.5	31	AA011631	Probe PM#78 corres
C	37	12	54.5	31	AA040308	Labelled probe CJ
C	38	12	54.5	32	AA092439	TCR beta constant
C	39	12	54.5	39	AA074788	Probe for stem cel
C	40	12	54.5	39	AA074794	Probe for Interleu
C	41	12	54.5	47	AA026715	Human map-related
C	42	12	54.5	50	AA076203	Human prostate spe
C	43	12	54.5	50	AA052277	Mouse ES cell nucl
C	44	11.8	53.6	18	AA064550	C-1027 gene cluste
C	45	11.8	53.6	20	AA021554	PCR primer used to

ALIGNMENTS

RESULT 1						
ID	AA041807/c	AA041807	standard; DNA; 24 BP.			
AC	AA041807;					
DT	03-SEP-1993	(first entry)				
DE	Baculovirus C2 complex binding site #4.					
KW	Myc; c-myc; mammalian; E box; cancer; therapy; C1; C2; C2'; complex;					
KW	homo-oligomer; hetero-oligomer; myogenin; Max; oncoprotein; primer;					
KW	probe; electrophoretic mobility shift assay; EMSA; ss.					
OS	Synthetic.					
FT	key	Location/Qualifiers				
FT	protein_bind	15..20				
FT	FT	/*tag= a				
FT	FT	/note= "C2 complex binding site"				
PN	WO9308701-A.					
XX						
PD	13-MAY-1993.					
XX						
PF	09-OCT-1992;	92WO-US08603.				
XX						
PR	30-OCT-1991;	91US-0785567.				
XX						
PA	(GENO) GEN HOSPITAL CORP.					
XX						
PI	Kingston RE, Papoulas O;					
XX						
DR	WPI; 1993-167291/20.					

XX Prodn. of c-Myc protein from mammalian cells - and detection of c-
 PT Myc inhibitors for use in cancer therapy
 XX
 PS Disclosure; Fig 7a; 101pp; English.
 XX
 CC The sequences given in AA041767-825 represent sequences which are
 CC bound in an electrophoretic mobility shift assay (EMSA) by Myc.
 CC The isolated sequences contain the central E box core of CACGTG which
 CC binds very weakly with Myc homo-oligomers (C1 complex), but more
 CC tightly with Myc hetero-oligomers (C2 complex). The C2 complex
 CC requires a 26-29 kD factor in addition to Myc. The additional factor
 CC copurifies with Myc and resembles Max protein. A second copurifying
 CC 40-50 kD factor has been identified (forming C2' complex). Sites
 CC selected by the C2' complex contain the core CACGTG which bears
 CC remarkable homology to a myogenin binding site (see AA041763).
 CC Oligonucleotides containing the E box can be used in the purification
 CC of Myc from a mammalian source. See also AA041761-861. The isolated
 CC target sequences may be used in a method to inhibit c-Myc oncoprotein
 CC activity.
 XX
 SO Sequence 24 BP; 8 A; 5 C; 8 G; 3 T; 0 other;

Query Match 69.1%; Score 15.2; DB 14; Length 24;
 Best Local Similarity 85.0%; Pred. No. 1.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 caccgcgtctctgcacatg 20
 ||| |||||
 Db 20 CACGTCGTCTCTCGACTATG 1

RESULT 2
 AAH46031/C
 ID AAH46031 standard; DNA; 45 BP.
 XX
 AC AAH46031;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE BCG derived synthetic oligonucleotide 5.
 XX
 KW Synthetic oligonucleotide; dinucleotide repeat; cytosstatic; apoptosis;
 KW cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;
 KW tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
 KW lymphoma; ss; BCG.
 XX
 OS Mycobacterium bovis.
 OS Synthetic.
 XX
 PN WO200144465-A2.
 XX
 PD 21-JUN-2001.
 XX
 PF 12-DEC-2000; 2000WO-CA01467.
 XX
 PR 13-DEC-1999; 99US-0170325.
 XX
 PR 29-AUG-2000; 2000US-0228925.
 XX
 PA (BION-) BIONICHE LIFE SCI INC.
 XX
 PI Phillips NC, Fillion MC;
 XX
 DR WPI: 2001-398150/42.
 XX
 PT Composition comprising synthetic oligonucleotides which comprise
 PT multiple repeats of dinucleotides such as GT, TG useful for treating
 PT cancer by inducing cell cycle arrest, inhibiting proliferation,
 PT activating caspases -
 XX
 PS Example 20; Page 34; 77pp; English.
 XX

CC The present sequence is that of a synthetic BCG (Bacillus
 CC Calmette-Guerin) derived oligonucleotide useful to the invention. The
 CC invention relates to a composition, comprising a 2 to 20 base 3'-OH,
 CC 5'-OH synthetic oligonucleotide which comprises multiple repeats of
 CC dinucleotides such as GT, TG, etc., according to specific formula and
 CC having cytostatic activity. The oligonucleotide compositions are useful
 CC for inducing cell cycle arrest, inhibition of proliferation, activation
 CC of caspases and induction of apoptosis or production of cytokines such as
 CC interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour necrosis factor
 CC (TNF)-alpha by immune system cells, in an animal having cancer such as
 CC primary carcinoma, secondary carcinoma, primary sarcoma and secondary
 CC sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal,
 CC ovarian or bone cancer. The compositions induce apoptosis independent of
 CC Fas, p53/p21, p21/waf-1/cip, p15(Ink4b), p16(Ink4), drug resistance,
 CC caspase 3, transforming growth factor (TGF)-beta 1 receptor and hormone
 CC dependence.
 XX
 SO Sequence 45 BP; 10 A; 17 C; 14 G; 4 T; 0 other;

Query Match 66.4%; Score 14.6; DB 22; Length 45;
 Best Local Similarity 81.0%; Pred. No. 2.9e+02;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 caccgcgtctctgcacatgg 21
 ||||| ||| |||||
 Db 30 CACCGCGCGCCCTCGACGATGG 10

RESULT 3
 AAH77485/C
 ID AAH77485 standard; cDNA; 51 BP.
 XX
 AC AAH77485;
 XX
 DT 16-NOV-2000 (first entry)
 XX
 DE Human gln synthase AT-ase-like gene polymorphic site, SEQ ID NO:1168.
 XX
 KW Human: single nucleotide polymorphism; SNP;
 KW detection; identification; gene therapy; ss.
 XX
 OS Homo sapiens.
 OS Key location/Qualifiers
 FH replace (26,C)
 FT variation /tag=a
 FT
 XX
 PN WO200029623-A2.
 XX
 PD 25-MAY-2000.
 XX
 PF 17-NOV-1999; 99WO-US27293.
 XX
 PR 17-NOV-1998; 98US-0109024.
 XX
 PR 16-NOV-1999; 99US-0109024.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shinkets RA, Leach MD;
 XX
 DR WPI: 2000-387826/33.
 XX
 DR P-PSDB; AAB11804.
 XX
 PT Human nucleic acids containing single nucleotide polymorphisms, useful
 PT for treating a subject suffering, or at risk from a pathology due to
 PT the presence of a sequence polymorphism -
 XX
 PS Claim 1; Page 511; 543pp; English.
 XX
 CC Sequences AAH76318-A77509 represent 1192 human nucleic acid sequences
 CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to
 CC 1112 (AAH76318-A77429) are consecutive pairs of nucleotides which

AA	AX23269		
ID	AA	AX23269 standard; DNA; 37 BP.	
XX	AC	AA	AX23269;
XX	DT	11-JUN-1999	(first entry)
XX	DE	Cytomegalovirus PCR primer ISOCMV002-AT	DNA.
XX	KW	Nucleic acid amplification; 3' overhang; strand displacing polymerase;	
KW	XX	isothermal; PCR primer; ss.	
OS	XX	Synthetic.	
OS	XX	Human cytomegalovirus.	
PN	XX	W09909211-A1.	
PD	XX	25-FEB-1999.	
PE	XX	12-AUG-1998;	98WO-GB02427.
PR	XX	13-AUG-1997;	97GB-0017061.
PA	XX	(TEPN-) TEPNEL MEDICAL LTD.	
PI	XX	Counts JC, Oultiram JD;	
DR	XX	WPI; 1999-190177/16.	
PT	XX	Amplifying a nucleic acid sequence by strand displacement - None	
PT	XX	given	
PS	XX	Example 4; Page 17; 41pp; English.	
CC	XX	This invention describes a novel method for amplifying a nucleic acid sequence of a double-stranded molecule, using a restriction enzyme which cuts to leave a 3' overhang on the strand not to be amplified, and strand displacing polymerase. The method allows nucleic acid amplification without the inclusion of a modified restriction site required in the prior art strand displacement method, and may be effected isothermally, unlike prior art polymerase chain reaction methods.	
CC	XX		
CC	XX	Sequence 37 BP; 9 A; 8 C; 9 G; 11 T; 0 other;	
SQ	XX		
Query Match 59.1%; Score 13; DB 20; Length 37;			
Best Local Similarity 76.2%; Pred. No. 1.8e+03;			
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;			
OY	2	accgcgtctctgcacaalga	22
DB	8	aaccactgtctcgacggtga	28
RESULT 9			
ID	AAA77484/C		
ID	AAA77484	standard; CDNA; 51 BP.	
AC	AAA77484;		
DT	16-NOV-2000	(first entry)	
DE	Human Gln synthase AT-ase-like gene polymorphic site, SEQ ID NO.1167.		
XX			
KW	Human; single nucleotide polymorphism; SNP;		
KW	detection; identification; gene therapy; ss.		
XX			
OS	Homo sapiens.		
XX			
Key	Location/Qualifiers		
FT	replace (26,T)		
FT	/*tag= a		

[illegible]

KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO950403-A2.
 XX
 PD 07-OCT-1999.
 XX
 PE 24-MAR-1999; 99MO-US06507.
 XX
 PR 27-MAR-1998; 98US-0079678.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Pavco PA, Roberts E, Jarvis T, Coesholt C, McSwigen JA;
 DR WPI; 1999-591315/50.
 XX
 PT Novel ribozymes for modulating the synthesis, expression and/or
 PT stability of an mRNA encoding an angiogenic factors
 XX
 PS Claim 53; Page 63; 305pp; English.

XX The present invention describes enzymatic cleavage of nucleic acid molecules with
 CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences. AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences.
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences.
 CC AAA21689 to AAA22475 and AAA23363 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23362, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding an angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (AMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiodioma of tuberosus sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 XX
 SQ Sequence 17 BP; 3 A; 5 C; 6 G; 3 U; 0 other;

Query Match 58.2%; Score 12.8; DB 20; Length 17;
 Best Local Similarity 87.5%; Pred. No. 2.1e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 gctctctgcacaatgg 21
 ||||| ||||| |||||
 Db 17 GCCCTCTGCAACAATG 2

RESULT 11
 AAV10088/c
 ID AAV10088 standard; DNA: 24 BP.
 XX
 AC AAV10088;
 XX
 DT 14-JUL-1998 (first entry)
 XX
 DE K-ras LDR oligonucleotide probe/primer Tet-K-ras c61.5E.
 XX
 KW Ligation assay; detection; ligase detection reaction; LDR; probe;

KW thermostable mutant ligase; cancer; mutation; forensic analysis;
 KW genetic disease; primer; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1
 FT /*tag-a
 FT /note="labelled with Tet"
 XX
 PN MO9803673-A1.
 XX
 PD 29-JAN-1998.
 XX
 PE 15-JUL-1997; 97MO-US12195.
 XX
 PR 19-JUL-1996; 96US-0022535.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 PA (PURD) PURDUE RES FOUND.
 XX
 PI Barany F, Bergstrom DE, Khanna M, Luo J;
 DR WPI; 1998-120792/11.
 XX
 PT Detecting minority nucleic acid in presence of larger amounts of
 PT closely related sequences - by ligase detection reaction with
 PT specific oligonucleotide probes, also thermostable mutant ligase and
 XX modified probes, used to detect cancer-related mutations
 XX
 PS Example 19; Fig 31B; 190pp; English.

XX The present sequence represents a ligase detection reaction (LDR)
 CC oligonucleotide probe used for the detection of K-ras codon 61, for use
 CC in present invention. The present invention describes a method for the
 CC detection of at least 1 minority target nucleic acid (I), present in a
 CC sample also containing majority nucleic target nucleic acids (II) and
 CC differing from (II) by at least 1 single-base change, insertion,
 CC deletion or translocation. The method comprises first treating the
 CC sample with: (a) ligase, and (b) at least 1 pair of target-specific
 CC oligonucleotide probes (A) which can be ligated together when hybridised
 CC adjacent to each other on their target sequence but have a mismatch that
 CC prevents ligation on any other sequence. The reaction mixture is
 CC subjected to at least 1 ligase detection reaction (LDR) cycle of
 CC denaturation, hybridisation and ligation, to produce a detectable
 CC ligation product that is distinguishable for each pair of probes. (A)
 CC may hybridise to other sequences but will not then be ligated and will
 CC be released during the denaturation step. The method is used to detect
 CC cancer-associated mutations in the presence of excess wild-type allele.
 CC The method can also be used to detect any bacterial, viral, fungal or
 CC parasitic infection (including drug-resistant strains) and many genetic
 CC diseases, it is also useful for environmental monitoring, forensic
 CC analysis and for identifying organisms/quality control in the food
 XX industry.

SQ Sequence 24 BP; 7 A; 5 C; 7 G; 5 T; 0 other;

Query Match 57.3%; Score 12.6; DB 19; Length 24;
 Best Local Similarity 76.9%; Pred. No. 2.7e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 caccgcctctcgcacaat 19
 ||||| ||||| ||||| |||||
 Db 24 CACCTGCTGTGTCGAGAAAT 6

RESULT 12
 AAX87183/c
 ID AAX87183 standard; DNA: 24 BP.
 XX
 AC AAX87183;
 XX

DT 27-SEP-1999 (first entry)
 XX Fibroblast growth factor receptor 1 gene PCR primer R/FGFR1/INTR.
 DE
 XX
 XX ZNF198-FCGR1, fibroblast growth factor receptor 1; oncogene;
 KW lymphoma; leukaemia; SCLL; translocation; stem cell; diagnosis;
 KW therapy; zinc finger protein; PCR; primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN W09935159-A1.
 XX
 PD 15-JUL-1999.
 XX
 PF 07-JAN-1999; 99WO-US00365.
 XX
 PR 08-JAN-1998; 98US-0004688.
 XX
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 XX
 PI Fletcher JA, Xiao S;
 XX
 DR WPI: 1999-430381/36.
 XX
 PT Oncogene, designated ZNF198-FCGR1, useful in diagnosis of stem cell
 PT leukemia and lymphoma syndrome
 XX
 PS Example; Page 65; 76pp; English.
 XX
 CC This primer oligonucleotide, designated F/FGFR1/INTR, is based on
 CC an intron region of the human fibroblast growth factor receptor 1
 CC (FCGR1) gene. It can be used for the PCR amplification of FCGR1
 CC nucleic acid sequences, especially to identify a newly discovered
 CC oncogene, ZNF198-FCGR1 (see AAX87177), which incorporates a FCGR1
 CC tyrosine kinase domain fused through t(8;13) translocation to
 CC ZNF198, and which is associated with stem cell leukaemia/lymphoma
 CC (SCLL) syndrome. The presence of ZNF198-FCGR1 nucleic acid in a
 CC tissue or fluid sample from a patient is indicative of SCLL
 CC syndrome.
 CC
 XX
 SQ Sequence 24 BP; 6 A; 7 C; 6 G; 5 T; 0 other;

Query Match 57.3%; Score 12.6; DB 20; Length 24;
 Best Local Similarity 78.9%; Pred. No. 2.7e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ccgcctctcgacatgga 22
 ||||| || |||||
 DB 24 CCGCTCTGTGCAAGATGGA 6

RESULT 13
 AAX23266
 ID AAX23266 standard; DNA; 37 BP.
 XX
 AC AAX23266;
 XX
 DT 11-JUN-1999 (first entry)
 XX
 DE Cytomegalovirus PCR primer ISOCMV002 DNA.
 XX
 KW Nucleic acid amplification; 3' overhang; strand displacing polymerase;
 KW Isothermal; PCR primer; ss.
 XX
 OS Synthetic.
 OS Human cytomegalovirus.
 XX
 PN W09909211-A1.
 XX
 PD 25-FEB-1999.

PF 12-AUG-1998; 98WO-GB02427.
 XX
 PR 13-AUG-1997; 97GB-0017061.
 XX
 PA (TEPN-) TEPNEL MEDICAL LTD.
 XX
 PI Coutts JC, Oultram JD;
 XX
 DR WPI: 1999-190177/16.
 XX
 PT Amplifying a nucleic acid sequence by strand displacement - None
 PT given
 XX
 PS Example 2; Page 14; 41pp; English.
 XX
 CC This invention describes a novel method for amplifying a nucleic acid
 CC sequence of a double-stranded molecule, using a restriction enzyme
 CC which cuts to leave a 3' overhang on the strand not to be amplified, and
 CC strand displacing polymerase. The method allows nucleic acid
 CC amplification without the inclusion of a modified restriction site
 CC required in the prior art strand displacement method, and may be
 CC effected isothermally, unlike prior art polymerase chain reaction
 CC methods.
 CC
 XX
 SQ Sequence 37 BP; 6 A; 10 C; 10 G; 11 T; 0 other;

Query Match 57.3%; Score 12.6; DB 20; Length 37;
 Best Local Similarity 78.9%; Pred. No. 2.9e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ccgcctctcgacatgga 22
 ||||| ||||| |||||
 DB 10 ccacgcctctcgacggtgga 28

RESULT 14
 AAT33699/C
 ID AAT33699 standard; DNA; 32 BP.
 XX
 AC AAT33699;
 XX
 DT 28-MAY-1997 (first entry)
 XX
 DE Mycobacterium heat shock protein hsp65 gene fragment PCR primer.
 XX
 KW Tumour vaccine; heat shock antigen; HSA; polymerase chain reaction;
 KW PCR; ss.
 XX
 OS Synthetic.
 XX
 PN W09629093-A1.
 XX
 PD 26-SEP-1996.
 XX
 PF 16-MAR-1996; 96WO-EP01142.
 XX
 PR 22-MAR-1995; 95DE-4010344.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX
 PI Schweighoffer T;
 XX
 DR WPI: 1996-442949/44.
 XX
 PT Tumour vaccines contg. antigen for which immune response exists -
 PT made from autologous and/or allogenic tumour cells modified with
 PT antigens, which are transfected, esp. using recombinant DNA
 XX
 PS Example 1; Page 21; 51pp; German.
 XX
 CC Tumour vaccines which contain autologous and/or allogeneous tumour cells
 CC which are modified so that they contain at least one antigen for which

CC an immune response already exists, are claimed. The vaccines take
CC advantage of a well defined, already extant cell immune response in the
CC host to act against tumour cells. The antigen is preferably from
CC Mycobacterium heat shock protein hsp65. The PCR primers in AAT33699
CC and AAT33700 were used in the construction of a plasmid for
CC expressing hsp65 in mouse melanoma cells.
XX
SQ Sequence 32 BP; 6 A; 8 C; 12 G; 6 T; 0 other;

Query Match 56.4%; Score 12.4; DB 17; Length 32;
Best Local Similarity 72.7%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 caccgcgtctcgcagaatgga 22
||||| ||||| ||| |||
Db 24 CACCCCTCTGTAGACTCTAGA 3

RESULT 15

AAF28152
ID AAF28152 standard; DNA; 42 BP.

XX
AC AAF28152;

XX
DT 02-APR-2001 (first entry)

XX
DE Primer #5.

XX
KW Vesiculovirus; vaccine; infection; cancer; ss.

XX
OS Unidentified.

XX
PN US6168943-B1.

XX
PD 02-JAN-2001.

XX
PF 03-MAY-1996; 96US-0646695.

XX
PR 04-MAY-1995; 95US-0435032.

XX
PA (UYVA) UNIV YALE.

XX
PI Rose JK;

XX
DR WPI: 2001-136716/14.

XX
PT Producing recombinant replicable vesiculovirus, useful as vaccines for
PT treating or preventing microbial infections, comprises culturing a cell
PT containing a nucleic acid for the expression of vesiculovirus
PT antigenomic RNA -

XX
PS Disclosure; Column 42; 119pp; English.

XX
CC The present invention relates to producing a recombinant replicable
CC vesiculovirus. The method involves culturing a cell containing a first
CC recombinant nucleic acid that can be transcribed to produce an RNA
CC comprising a vesiculovirus antigenomic (+) RNA containing the
CC vesiculovirus promoter for replication and a ribozyme sequence
CC immediately downstream the antigenomic (+) RNA. The method is useful
CC for producing recombinant replicable vesiculoviruses, which can
CC be used as vaccines for the treatment or prevention of
CC infections by a pathogenic microorganism. The recombinant
CC replicable vesiculoviruses are useful in diagnosing and monitoring
CC progression of infectious disorders, including response to vaccination
CC and/or therapy, in cancer immunoprophylaxis, immunotherapy and
CC diagnosis, and monitoring of tumor progression or regression, and to
CC produce large quantities of readily purified antigen.
XX
SQ Sequence 42 BP; 14 A; 10 C; 12 G; 6 T; 0 other;

Query Match 56.4%; Score 12.4; DB 22; Length 42;

Best Local Similarity 72.7%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY 1 caccgcgtctcgcagaatgga 22
||||| ||||| ||| |||
Db 4 ccccgggctcgcagaatgga 25

Search completed: March 9, 2002, 01:07:00
Job time: 11946 sec

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)